

# Sequence Listing

<110> Genentech, Inc.  
 Ashkenazi, Avi J.  
 Fong, Sherman  
 Goddard, Audrey  
 Gurney, Austin L.  
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 Tumas, Daniel  
 Wood, William I.

<120> COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT  
 OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS

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 <141> 1999-03-05

<150> PCT/US98/24855  
 <151> 1998-11-20

<150> US 60/066,364  
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<150> US 60/078,936  
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<150> PCT/US98/19437  
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 Thr Tyr Thr Cys Met Val Ser Glu Glu Gly Gly Asn Ser Tyr Gly  
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Glu	Val	Lys	Val	Lys	Leu	Ile	Val	Leu	Val	Pro	Pro	Ser	Lys	Pro	125	130	135
Thr	Val	Asn	Ile	Pro	Ser	Ser	Ala	Thr	Ile	Gly	Asn	Arg	Ala	Val	140	145	150
Leu	Thr	Cys	Ser	Glu	Gln	Asp	Gly	Ser	Pro	Pro	Ser	Glu	Tyr	Thr	155	160	165
Trp	Phe	Lys	Asp	Gly	Ile	Val	Met	Pro	Thr	Asn	Pro	Lys	Ser	Thr	170	175	180
Arg	Ala	Phe	Ser	Asn	Ser	Ser	Tyr	Val	Leu	Asn	Pro	Thr	Thr	Gly	185	190	195
Glu	Leu	Val	Phe	Asp	Pro	Leu	Ser	Ala	Ser	Asp	Thr	Gly	Glu	Tyr	200	205	210
Ser	Cys	Glu	Ala	Arg	Asn	Gly	Tyr	Gly	Thr	Pro	Met	Thr	Ser	Asn	215	220	225
Ala	Val	Arg	Met	Glu	Ala	Val	Glu	Arg	Asn	Val	Gly	Val	Ile	Val	230	235	240
Ala	Ala	Val	Leu	Val	Thr	Leu	Ile	Leu	Leu	Gly	Ile	Leu	Val	Phe	245	250	255
Gly	Ile	Trp	Phe	Ala	Tyr	Ser	Arg	Gly	His	Phe	Asp	Arg	Thr	Lys	260	265	270
Lys	Gly	Thr	Ser	Ser	Lys	Lys	Val	Ile	Tyr	Ser	Gln	Pro	Ser	Ala	275	280	285
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Leu	Leu	Phe	Lys	Pro	Ala	Val	Ile	Ala	Asp	Ser	Gly	Ser	Tyr	Phe
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Cys	Thr	Ala	Lys	Gly	Gln	Val	Gly	Ser	Glu	Gln	His	Ser	Asp	Ile
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Val	Lys	Phe	Val	Val	Lys	Asp	Ser	Ser	Lys	Leu	Leu	Lys	Thr	Lys
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Thr	Glu	Ala	Pro	Thr	Thr	Met	Thr	Tyr	Pro	Leu	Lys	Ala	Thr	Ser
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Thr	Val	Lys	Gln	Ser	Trp	Asp	Trp	Thr	Thr	Asp	Met	Asp	Gly	Tyr
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Leu	Gly	Glu	Thr	Ser	Ala	Gly	Pro	Gly	Lys	Ser	Leu	Pro	Val	Phe
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Ala	Ile	Ile	Leu	Ile	Ile	Ser	Leu	Cys	Cys	Met	Val	Val	Phe	Thr
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Met	Ala	Tyr	Ile	Met	Leu	Cys	Arg	Lys	Thr	Ser	Gln	Gln	Glu	His
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Leu	Glu	Trp	Lys	Lys	Leu	Gly	Arg	Ser	Val	Ser	Phe	Val	Tyr	Tyr
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Thr	Ser	Phe	Gln	Lys	Ser	Asn	Ser	Ser	Ser	Lys	Ala	Thr	Thr	Met	275	280	285
Ser	Glu	Asn	Val	Gln	Trp	Leu	Thr	Pro	Val	Ile	Pro	Ala	Leu	Trp	290	295	300
Lys	Ala	Ala	Ala	Gly	Gly	Ser	Arg	Gly	Gln	Glu	Phe				305	310	

<210> 10  
 <211> 300  
 <212> PRT  
 <213> Mus musculus

Met	Gly	Thr	Glu	Gly	Lys	Ala	Gly	Arg	Lys	Leu	Leu	Phe	Leu	Phe	1	5	10	15
Thr	Ser	Met	Ile	Leu	Gly	Ser	Leu	Val	Gln	Gly	Lys	Gly	Ser	Val	20	25	30	
Tyr	Thr	Ala	Gln	Ser	Asp	Val	Gln	Val	Pro	Glu	Asn	Glu	Ser	Ile	35	40	45	
Lys	Leu	Thr	Cys	Thr	Tyr	Ser	Gly	Phe	Ser	Ser	Pro	Arg	Val	Glu	50	55	60	
Trp	Lys	Phe	Val	Gln	Gly	Ser	Thr	Thr	Ala	Leu	Val	Cys	Tyr	Asn	65	70	75	
Ser	Gln	Ile	Thr	Ala	Pro	Tyr	Ala	Asp	Arg	Val	Thr	Phe	Ser	Ser	80	85	90	
Ser	Gly	Ile	Thr	Phe	Ser	Ser	Val	Thr	Arg	Lys	Asp	Asn	Gly	Glu	95	100	105	
Tyr	Thr	Cys	Met	Val	Ser	Glu	Glu	Gly	Gly	Gln	Asn	Tyr	Gly	Glu	110	115	120	

Val	Ser	Ile	His	Leu	Thr	Val	Leu	Val	Pro	Pro	Ser	Lys	Pro	Thr
				125					130					135
Ile	Ser	Val	Pro	Ser	Ser	Val	Thr	Ile	Gly	Asn	Arg	Ala	Val	Leu
				140					145					150
Thr	Cys	Ser	Glu	His	Asp	Gly	Ser	Pro	Pro	Ser	Glu	Tyr	Ser	Trp
				155					160					165
Phe	Lys	Asp	Gly	Ile	Ser	Met	Leu	Thr	Ala	Asp	Ala	Lys	Lys	Thr
				170					175					180
Arg	Ala	Phe	Met	Asn	Ser	Ser	Phe	Thr	Ile	Asp	Pro	Lys	Ser	Gly
				185					190					195
Asp	Leu	Ile	Phe	Asp	Pro	Val	Thr	Ala	Phe	Asp	Ser	Gly	Glu	Tyr
				200					205					210
Tyr	Cys	Gln	Ala	Gln	Asn	Gly	Tyr	Gly	Thr	Ala	Met	Arg	Ser	Glu
				215					220					225
Ala	Ala	His	Met	Asp	Ala	Val	Glu	Leu	Asn	Val	Gly	Gly	Ile	Val
				230					235					240
Ala	Ala	Val	Leu	Val	Thr	Leu	Ile	Leu	Leu	Gly	Leu	Leu	Ile	Phe
				245					250					255
Gly	Val	Trp	Phe	Ala	Tyr	Ser	Arg	Gly	Tyr	Phe	Glu	Thr	Thr	Lys
				260					265					270
Lys	Gly	Thr	Ala	Pro	Gly	Lys	Lys	Val	Ile	Tyr	Ser	Gln	Pro	Ser
				275					280					285
Thr	Arg	Ser	Glu	Gly	Glu	Phe	Lys	Gln	Thr	Ser	Ser	Phe	Leu	Val
				290					295					300

<210> 11  
 <211> 2181  
 <212> DNA  
 <213> Homo sapiens

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 ccaccagaag tttgagcctc tttggtagca ggaggctgga agaaaggaca 100  
 gaagtagctc tggtgtgat ggggatctta ctgggcctgc tactcctggg 150  
 gcacctaaac gtggacactt atggccgtcc catcctggaa gtgccagaga 200  
 gtgtaacagg accttggaac ggggatgtga atcttcctg cacctatgac 250  
 ccctgcaag gctacacca agtcttggtg aagtggctgg tacaacgtgg 300  
 ctcagaccct gtcaccatct ttctacgtga ctcttctgga gaccatatcc 350  
 agcaggcaaa gtaccagggc cgctgcatg tgagccacaa ggttccagga 400  
 gatgtatccc tccaattgag caccctggag atggatgacc ggagccacta 450  
 cacgtgtgaa gtcacctggc agactcctga tggcaaccaa gtcgtgagag 500  
 ataagattac tgagctccgt gtccagaaac tctctgtctc caagcccaca 550

gtgacaactg gcagcgggta tggcttcacg gtgccccagg gaatgaggat 600  
 tagccttcaa tgccaggctc ggggtttctc tcccatcagt tatatttggg 650  
 ataagcaaca gactaataac caggaacca tcaaagtagc aaccctaagt 700  
 accttactct tcaagcctgc ggtgatagcc gactcaggct cctatttctg 750  
 cactgccaag ggccagggtg gctctgagca gcacagcgac attgtgaagt 800  
 ttgtgggtcaa agactcctca aagctactca agaccaagac tgaggcacct 850  
 acaaccatga cataccctt gaaagcaaca tctacagtga agcagtcctg 900  
 ggactggacc actgacatgg atggctacct tggagagacc agtgctgggc 950  
 caggaaagag cctgcctgtc tttgccatca tctcatcat ctcttgtgc 1000  
 tgtatggtgg tttttaccat ggcctatata atgctctgtc ggaagacata 1050  
 ccaacaagag catgtctacg aagcagccag gtaagaaagt ctctctctt 1100  
 ccatttttga ccccgctcct gccctcaatt ttgattactg gcaggaaatg 1150  
 tggaggaagg ggggtgtggc acagacccaa tcctaaggcc ggaggccttc 1200  
 agggtcagga catagctgcc ttcctctctc caggcacctt ctgaggttgt 1250  
 tttggccctc tgaacacaaa ggataattta gatccatctg ccttctgctt 1300  
 ccagaatccc tgggtggtag gatcctgata attaatggc aagaattgag 1350  
 gcagaagggg gggaaaccag gaccacagcc ccaagtccct tcttatgggt 1400  
 ggtgggctct tgggcatag ggcacatgcc agagaggcca acgactctgg 1450  
 agaaaccatg aggggtggcca tcttcgcaag tggctgctcc agtgatgagc 1500  
 caacttccca gaatctgggc aacaactact ctgatgagcc ctgcatagga 1550  
 caggagtacc agatcatcgc ccagatcaat ggcaactacg cccgcctgct 1600  
 ggacacagtt cctctggatt atgagtttct ggccactgag ggcaaaagt 1650  
 tctgttaaaa atgccccatt aggccaggat ctgctgacat aattgcctag 1700  
 tcagtccttg ccttctgcat ggccttcttc cctgctacct ctcttctgg 1750  
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 ctttgccttg gaatttgcca gatgcatctc aagtaagcca gctgctggat 1850  
 ttggctctgg gcccttctag tatctctgcc gggggcttct ggtactctc 1900  
 tctaaatacc agagggaaga tgcccatagc actaggactt ggtcatcatg 1950  
 cctacagaca ctattcaact ttggcatctt gccaccagaa gacccgaggg 2000  
 aggctcagct ctgccagctc agaggaccag ctatatccag gatcatttct 2050  
 ctttcttcag ggccagacag cttttaattg aaattgttat ttcacaggcc 2100  
 agggttcagt tctgtctctc cactataagt ctaatgttct gactctctcc 2150

tgggtgctcaa taaatatcta atcataacag c 2181  
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 <211> 50  
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 <212> DNA  
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 <400> 14  
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 <210> 15  
 <211> 24  
 <212> DNA  
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 <400> 15  
 taggaagagt tgctgaaggc acgg 24  
 <210> 16  
 <211> 20  
 <212> DNA  
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 <220>  
 <223> artificial sequence  
 <400> 16  
 ttgccttact caggtgctac 20  
 <210> 17  
 <211> 20  
 <212> DNA  
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<400> 17  
actcagcagt ggtaggaaag 20

<210> 18  
<211> 24  
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<220>  
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<400> 18  
tatccctcca attgagcacc ctgg 24

<210> 19  
<211> 21  
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<220>  
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<400> 19  
gtcggaagac atcccaacaa g 21

<210> 20  
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<400> 20  
cttcacaatg tcgctgtgct gctc 24

<210> 21  
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<400> 21  
agccaaatcc agcagctggc ttac 24

<210> 22  
<211> 50  
<212> DNA  
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<220>  
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<400> 22  
tggatgaccg gagccactac acgtgtgaag tcacctggca gactcctgat 50

<210> 23  
<211> 260  
<212> PRT

<213> Homo sapiens

<400> 23

Leu	Ala	Leu	Gly	Ser	Val	Thr	Val	His	Ser	Ser	Glu	Pro	Glu	Val	
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Arg	Ile	Pro	Glu	Asn	Asn	Pro	Val	Lys	Leu	Ser	Cys	Ala	Tyr	Ser	
				20					25					30	
Gly	Phe	Ser	Ser	Pro	Arg	Val	Glu	Trp	Lys	Phe	Asp	Gln	Gly	Asp	
				35					40					45	
Thr	Thr	Arg	Leu	Val	Cys	Tyr	Asn	Asn	Lys	Ile	Thr	Ala	Ser	Tyr	
				50					55					60	
Glu	Asp	Arg	Val	Thr	Phe	Leu	Pro	Thr	Gly	Ile	Thr	Phe	Lys	Ser	
				65					70					75	
Val	Thr	Arg	Glu	Asp	Thr	Gly	Thr	Tyr	Thr	Cys	Met	Val	Ser	Glu	
				80					85					90	
Glu	Gly	Gly	Asn	Ser	Tyr	Gly	Glu	Val	Lys	Val	Lys	Leu	Ile	Val	
				95					100					105	
Leu	Val	Pro	Pro	Ser	Lys	Pro	Thr	Val	Asn	Ile	Pro	Ser	Ser	Ala	
				110					115					120	
Thr	Ile	Gly	Asn	Arg	Ala	Val	Leu	Thr	Cys	Ser	Glu	Gln	Asp	Gly	
				125					130					135	
Ser	Pro	Pro	Ser	Glu	Tyr	Thr	Trp	Phe	Lys	Asp	Gly	Ile	Val	Met	
				140					145					150	
Pro	Thr	Asn	Pro	Lys	Ser	Thr	Arg	Ala	Phe	Ser	Asn	Ser	Ser	Tyr	
				155					160					165	
Val	Leu	Asn	Pro	Thr	Thr	Gly	Glu	Leu	Val	Phe	Asp	Pro	Leu	Ser	
				170					175					180	
Ala	Ser	Asp	Thr	Gly	Glu	Tyr	Ser	Cys	Glu	Ala	Arg	Asn	Gly	Tyr	
				185					190					195	
Gly	Thr	Pro	Met	Thr	Ser	Asn	Ala	Val	Arg	Met	Glu	Ala	Val	Glu	
				200					205					210	
Arg	Asn	Val	Gly	Val	Ile	Val	Ala	Ala	Val	Leu	Val	Thr	Leu	Ile	
				215					220					225	
Leu	Leu	Gly	Ile	Leu	Val	Phe	Gly	Ile	Trp	Phe	Ala	Tyr	Ser	Arg	
				230					235					240	
Gly	His	Phe	Asp	Arg	Thr	Lys	Lys	Gly	Thr	Ser	Ser	Lys	Lys	Val	
				245					250					255	
Ile	Tyr	Ser	Gln	Pro											
				260											

<210> 24

<211> 270

<212> PRT

<213> Homo sapiens

<400> 24

Val	Arg	Val	Thr	Val	Asp	Ala	Ile	Ser	Val	Glu	Thr	Pro	Gln	Asp	
1				5					10					15	
Val	Leu	Arg	Ala	Ser	Gln	Gly	Lys	Ser	Val	Thr	Leu	Pro	Cys	Thr	
				20					25					30	
Tyr	His	Thr	Ser	Thr	Ser	Ser	Arg	Glu	Gly	Leu	Ile	Gln	Trp	Asp	
				35					40					45	
Lys	Leu	Leu	Leu	Thr	His	Thr	Glu	Arg	Val	Val	Ile	Trp	Pro	Phe	
				50					55					60	
Ser	Asn	Lys	Asn	Tyr	Ile	His	Gly	Glu	Leu	Tyr	Lys	Asn	Arg	Val	
				65					70					75	
Ser	Ile	Ser	Asn	Asn	Ala	Glu	Gln	Ser	Asp	Ala	Ser	Ile	Thr	Ile	
				80					85					90	
Asp	Gln	Leu	Thr	Met	Ala	Asp	Asn	Gly	Thr	Tyr	Glu	Cys	Ser	Val	
				95					100					105	
Ser	Leu	Met	Ser	Asp	Leu	Glu	Gly	Asn	Thr	Lys	Ser	Arg	Val	Arg	
				110					115					120	
Leu	Leu	Val	Leu	Val	Pro	Pro	Ser	Lys	Pro	Glu	Cys	Gly	Ile	Glu	
				125					130					135	
Gly	Glu	Thr	Ile	Ile	Gly	Asn	Asn	Ile	Gln	Leu	Thr	Cys	Gln	Ser	
				140					145					150	
Lys	Glu	Gly	Ser	Pro	Thr	Pro	Gln	Tyr	Ser	Trp	Lys	Arg	Tyr	Asn	
				155					160					165	
Ile	Leu	Asn	Gln	Glu	Gln	Pro	Leu	Ala	Gln	Pro	Ala	Ser	Gly	Gln	
				170					175					180	
Pro	Val	Ser	Leu	Lys	Asn	Ile	Ser	Thr	Asp	Thr	Ser	Gly	Tyr	Tyr	
				185					190					195	
Ile	Cys	Thr	Ser	Ser	Asn	Glu	Glu	Gly	Thr	Gln	Phe	Cys	Asn	Ile	
				200					205					210	
Thr	Val	Ala	Val	Arg	Ser	Pro	Ser	Met	Asn	Val	Ala	Leu	Tyr	Val	
				215					220					225	
Gly	Ile	Ala	Val	Gly	Val	Val	Ala	Ala	Leu	Ile	Ile	Ile	Gly	Ile	
				230					235					240	
Ile	Ile	Tyr	Cys	Cys	Cys	Cys	Arg	Gly	Lys	Asp	Asp	Asn	Thr	Glu	
				245					250					255	
Asp	Lys	Glu	Asp	Ala	Arg	Pro	Asn	Arg	Glu	Ala	Tyr	Glu	Glu	Pro	
				260					265					270	

<210> 25

<211> 263

<212> PRT

<213> Homo sapiens

<400> 25

Leu	Cys	Ser	Leu	Ala	Leu	Gly	Ser	Val	Thr	Val	His	Ser	Ser	Glu	
1				5					10					15	

Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu Ser Cys  
 20 25 30  
 Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe Asp  
 35 40 45  
 Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr  
 50 55 60  
 Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr  
 65 70 75  
 Phe Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met  
 80 85 90  
 Val Ser Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys  
 95 100 105  
 Leu Ile Val Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro  
 110 115 120  
 Ser Ser Ala Thr Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu  
 125 130 135  
 Gln Asp Gly Ser Pro Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly  
 140 145 150  
 Ile Val Met Pro Thr Asn Pro Lys Ser Thr Arg Ala Phe Ser Asn  
 155 160 165  
 Ser Ser Tyr Val Leu Asn Pro Thr Thr Gly Glu Leu Val Phe Asp  
 170 175 180  
 Pro Leu Ser Ala Ser Asp Thr Gly Glu Tyr Ser Cys Glu Ala Arg  
 185 190 195  
 Asn Gly Tyr Gly Thr Pro Met Thr Ser Asn Ala Val Arg Met Glu  
 200 205 210  
 Ala Val Glu Arg Asn Val Gly Val Ile Val Ala Ala Val Leu Val  
 215 220 225  
 Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly Ile Trp Phe Ala  
 230 235 240  
 Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly Thr Ser Ser  
 245 250 255  
 Lys Lys Val Ile Tyr Ser Gln Pro  
 260

<210> 26

<211> 273

<212> PRT

<213> Homo sapiens

<400> 26

Leu Cys Ala Val Arg Val Thr Val Asp Ala Ile Ser Val Glu Thr  
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Pro Gln Asp Val Leu Arg Ala Ser Gln Gly Lys Ser Val Thr Leu  
 20 25 30

Pro	Cys	Thr	Tyr	His	Thr	Ser	Thr	Ser	Ser	Arg	Glu	Gly	Leu	Ile	
				35					40					45	
Gln	Trp	Asp	Lys	Leu	Leu	Leu	Thr	His	Thr	Glu	Arg	Val	Val	Ile	
				50					55					60	
Trp	Pro	Phe	Ser	Asn	Lys	Asn	Tyr	Ile	His	Gly	Glu	Leu	Tyr	Lys	
				65					70					75	
Asn	Arg	Val	Ser	Ile	Ser	Asn	Asn	Ala	Glu	Gln	Ser	Asp	Ala	Ser	
				80					85					90	
Ile	Thr	Ile	Asp	Gln	Leu	Thr	Met	Ala	Asp	Asn	Gly	Thr	Tyr	Glu	
				95					100					105	
Cys	Ser	Val	Ser	Leu	Met	Ser	Asp	Leu	Glu	Gly	Asn	Thr	Lys	Ser	
				110					115					120	
Arg	Val	Arg	Leu	Leu	Val	Leu	Val	Pro	Pro	Ser	Lys	Pro	Glu	Cys	
				125					130					135	
Gly	Ile	Glu	Gly	Glu	Thr	Ile	Ile	Gly	Asn	Asn	Ile	Gln	Leu	Thr	
				140					145					150	
Cys	Gln	Ser	Lys	Glu	Gly	Ser	Pro	Thr	Pro	Gln	Tyr	Ser	Trp	Lys	
				155					160					165	
Arg	Tyr	Asn	Ile	Leu	Asn	Gln	Glu	Gln	Pro	Leu	Ala	Gln	Pro	Ala	
				170					175					180	
Ser	Gly	Gln	Pro	Val	Ser	Leu	Lys	Asn	Ile	Ser	Thr	Asp	Thr	Ser	
				185					190					195	
Gly	Tyr	Tyr	Ile	Cys	Thr	Ser	Ser	Asn	Glu	Glu	Gly	Thr	Gln	Phe	
				200					205					210	
Cys	Asn	Ile	Thr	Val	Ala	Val	Arg	Ser	Pro	Ser	Met	Asn	Val	Ala	
				215					220					225	
Leu	Tyr	Val	Gly	Ile	Ala	Val	Gly	Val	Val	Ala	Ala	Leu	Ile	Ile	
				230					235					240	
Ile	Gly	Ile	Ile	Ile	Tyr	Cys	Cys	Cys	Cys	Arg	Gly	Lys	Asp	Asp	
				245					250					255	
Asn	Thr	Glu	Asp	Lys	Glu	Asp	Ala	Arg	Pro	Asn	Arg	Glu	Ala	Tyr	
				260					265					270	

Glu Glu Pro

<210> 27

<211> 413

<212> DNA

<213> artificial sequence

<220>

<223> artificial sequence

<400> 27

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catctgagca aggccaaaac ctggaagagg atacagtcac tctggaagta 100

ttagtggtc cagcagttcc atcatgtgaa gtaccctctt ctgctctgag 150  
tggaactgtg gtagagctac gatgtcaaga caaagaaggg aatccagctc 200  
ctgaatacac atgggtttaag gatggcatcc gtttgctaga aaatcccaga 250  
cttggtccc aaagcaccaa cagctcatat acaatgaata caaaaactgg 300  
aactctgcaa ttttaactg tttccaaact ggacactgga gaatattcct 350  
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gcaagtagat gat 413

<210> 28  
<211> 22  
<212> DNA  
<213> artificial sequence

<220>  
<223> artificial sequence

<400> 28  
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<210> 29  
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<212> DNA  
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<220>  
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<400> 29  
acctgcgata tccaacagaa ttg 23

<210> 30  
<211> 48  
<212> DNA  
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<220>  
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<400> 30  
ggaagaggat acagtcactc tggaagtatt agtggctcca gcagttcc 48